



PCT

## RAW SEQUENCE LISTING

DATE: 10/05/2004

PATENT APPLICATION: US/10/509,422

TIME: 11:16:59

Input Set : A:\Attorney Docket No. 004974.01054 sequence listing.txt.TXT

Output Set: N:\CRF4\10052004\J509422.raw

6 <110> APPLICANT: Liou, Simon  
 8 <120> TITLE OF INVENTION: Human BMP2 Inducible Kinases  
 10 <130> FILE REFERENCE: 004974.01015  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/509,422  
 C--> 12 <141> CURRENT FILING DATE: 2004-09-24  
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP03/080825  
 13 <151> PRIOR FILING DATE: 2003-03-20  
 15 <150> PRIOR APPLICATION NUMBER: US 60/367,512  
 16 <151> PRIOR FILING DATE: 2002-03-27  
 18 <150> PRIOR APPLICATION NUMBER: US 60/406,936  
 19 <151> PRIOR FILING DATE: 2002-08-30  
 21 <160> NUMBER OF SEQ ID NOS: 9  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0

**Does Not Comply  
 Corrected Diskette Needed!**

## ERRORED SEQUENCES

245 <210> SEQ ID NO: 3  
 246 <211> LENGTH: 3704  
 247 <212> TYPE: DNA  
 248 <213> ORGANISM: Homo sapiens  
 E--> 250 <400> SEQUENCE: ④ 3 ← change to  
 251 cgggccaggg gcggcgaccc ctgcgagacg cccggctgcg cgccggggccg gggacttgcc 60  
 252 cttgcacgct ccctgcgccc tccagctcgc cggcgggacc atgaagaagt tctctcggat 120  
 253 gcccaagtcg gagggcgga gcggcgggcg agcgcggggt ggcggggctg gcggggccgg 180  
 254 ggccggggcc ggctgcggct ccggcgggctc gtccgtgggg gtccgggtgt tcgcggtcgg 240  
 255 ccgccaccag gtcaccctgg aagagtcgct ggccgaaggt ggattctcca cagttttcct 300  
 256 cgtgcgtact cacgggtgaa tccgatgtgc attgaagcga atgtatgtca ataacatgcc 360  
 257 agacctcaat gtttgtaaaa gggaaattac aattatgaaa gagctatctg gtcacaaaaa 420  
 258 tattgtgggc tatttggtact gtgctgttaa ttcaattagt gataatgtat ggggaagtcct 480  
 259 tatcttaatg gaattattgtc gagctggaca ggtagtgaat caaatgaata agaagctaca 540  
 260 gacgggtttt acagaaccag aagtgttaca gatattctgt gataacctgt aagctgttgc 600  
 261 aagggttgcag cagtgtgaaga ctccaataat tcaccgggat ctgaaggtag aaaatatttt 660  
 262 gttgaatgat ggtgggaact atgtactttg tgactttggc agtgccacta ataaatttct 720  
 263 taatcctcaa aaagatggag ttaatgtagt agaagaagaa attaaaaagt atacaactct 780  
 264 gtcatacaga gccctgaaa tgatcaacct ttatggaggg aaacccatca ccaccaaggc 840  
 265 tgatatctgg gcaactggat gtctactcta taaactttgt ttcttcactc ttctttttgg 900  
 266 tgagagtcag gttgctatct gtgatggcaa cttcaccatc ccagacaatt ctcgttactc 960  
 267 ccgtaacata cattgcttaa taaggttcat gcttgaacca gatccggaac atagacctga 1020  
 268 tatattttcaa gtgtcatatt ttgcatttaa atttgccaaa aaggattgtc cagtctccaa 1080  
 269 catcaataat tcttctatct cttcagctct tcctgaaccg atgactgcta gtgaagcagc 1140  
 270 tgctaggaaa agccaaataa aagccagaat aacagatacc attggacca cagaaacctc 1200  
 271 aattgcacca agacaaagac caaaggccaa ctctgctact actgccactc ccagtggtgt 1260

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272 gaccattcaa agttcagcaa cacctgttaa agtccttgct cctggtgaat tccgtaacca 1320
273 tagacaaaaa ggggcactaa gacctggaaa tggccctgaa attttattgg gtcagggacc 1380
274 tcctcagcag ccgccacagc agcatagagt actccagcaa ctacagcagg gagattggag 1440
275 attacagcaa ctccatttac agcatcgtca tcctcaccag cagcagcagc agcagcagca 1500
276 gcaacagcaa cagcagcagc agcaacagca acagcagcag cagcagcagc agcagcagca 1560
277 ccaccaccac caccaccacc acctacttca agatgcttat atgcagcagt atcaacatgc 1620
278 aacacagcag caacagatgc ttcaacaaca atttttaatg cattcggtat atcaaccaca 1680
279 accttctgca tcacagtatc ctacaatgat gccgcagtat cagcaggcct tctttcaaca 1740
280 gcagatgcta gctcaacatc agccgtctca acaacaggca tcacctgaat atcttacctc 1800
281 cctcaagag ttctcaccag ccttagtttc ctacacttca tcacttccag ctgaggttgg 1860
282 aaccataatg gactcctcct atagtgccaa taggcaagta tttttccagt cagttgctga 1920
283 taaagaggcc attgcaaatt tcacaaatca gaagaacatc agcaatccac ctgatatgtc 1980
284 aggggtggaat ctttttggag aggataatct ctctaagtta acagaagagg aactattgga 2040
285 cagagaatct gaccttctaa gatcaaatag gctcgaggag agagcatcct cagataagaa 2100
286 tgtagactca ctttctgctc cacataacca tcctccagaa gatccttttg gttctgttcc 2160
287 tttcatttct cattcaggca agggttctcc tgaaaagaaa gctgaacatt catctataaa 2220
288 tcaagaaaat ggcactgcaa accctatcaa gaacggtaaa acaagtccag catctaaaga 2280
289 tcagcggact ggaaagaaaa cctcagtaca gggcgaagtg caaaagggga atgatgaatc 2340
290 tgaaagtgat tttgaatcag atcccccttc tcctaagagc agtgaagagg aagagcaaga 2400
291 tgatgaagaa gttcttcagg gggaacaagg agattttaat gatgatgata ctgaaccaga 2460
292 aaatctgggt cataggcctc tcctcatgga ttctgaagat gaggaagaag aggagaaaca 2520
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294 cagagacaga tctggcagtg gaccaacca agatcttaac acaatactcc tcacctcagc 2640
295 ccaattatcc tctgatgttg cagtggagac tcccaaacag gagtttgatg tatttggcgc 2700
296 tgtccccttc tttgcagtg cgtctcaaca gcccagcaa gaaaagaatg aaaagaacct 2760
297 cctcaacac aggtttcctg ctgcaggact ggagcaggag gaatttgatg tattcacaaa 2820
298 ggcgcctttt agcaagaagg tgaatgtaca agaatgccat gcagtggggc ctgaggcaca 2880
299 tactatccct ggttatccca aaagtgtaga tgtatttggc tccactccat ttcagccctt 2940
300 cctcacatca acaagtaaaa gtgaaagcaa tgaggacctt tttgggcttg tgccctttga 3000
301 tgaaataacg gggagccagc agcaaaaagt caaacagcgc agcttacaga aactgtcctc 3060
302 tcgccaaagg cgcacaaagc aggatatgtc caaaagtaat ggggaagcggc atcatggcac 3120
303 gccaaactagc acaaagaaga ctttgaagcc tacctatcgc actccagaga gggctcgcag 3180
304 gcacaaaaaa gtgggcccgc gagactctca aagtagcaat gaatttttaa ccatctcaga 3240
305 ctccaaggag aacattagt tggcactgac tgatgggaaa gataggggga atgtcttaca 3300
306 acctgaggag agcctgttgg accccttcgg tgccaagccc ttccattctc cagacctgtc 3360
307 atggcacctt ccacatcagg gctgagcga catccgtgct gatcacaata ctgtcctgcc 3420
308 agggcgccca agacaaaatt cactacatgg gtcattccat agtgcagatg tattgaaat 3480
309 ggatgatttt ggtgccgtgc cctttacaga acttgtgggtg caaagcatca ctccacatca 3540
310 gtcccaacag tcccaaccag tcgaattaga cccatttggg gctgtcccat ttccttctaa 3600
311 acagtagata cttctgatgg attctcggca ttaactcctg tttcaaaaaa gtgtgaacag 3660
312 ttttatgaat ttgaaagaaa atttggtagc tctttatagc attc 3704

```

317 &lt;210&gt; SEQ ID NO: 4

318 &lt;211&gt; LENGTH: 1138

319 &lt;212&gt; TYPE: PRT

320 &lt;213&gt; ORGANISM: Mus musculus

E--&gt; 322 &lt;400&gt; SEQUENCE: 3046

323 Met Lys Lys Phe Ser Arg Met Pro Lys Ser Glu Gly Ser Gly Gly Gly

324 1 5 10 15

325 Ala Ala Ala Gly Gly Ala Ala Gly Gly Gly Leu Gly Gly Gly Phe Ala

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```

326          20          25          30
327 Ser Ser Ser Met Gly Val Arg Val Phe Ala Val Gly Arg Tyr Gln Val
328          35          40          45
329 Thr Leu Glu Glu Ser Leu Ala Glu Gly Gly Phe Ser Thr Val Phe Leu
330          50          55          60
331 Val Arg Thr His Ser Gly Ile Arg Cys Ala Leu Lys Arg Met Tyr Val
332 65          70          75          80
333 Asn Asn Thr Pro Asp Leu Asn Ile Cys Lys Arg Glu Ile Thr Ile Met
334          85          90          95
335 Lys Glu Leu Ser Gly His Lys Asn Ile Val Gly Tyr Leu Asp Cys Ala
336          100          105          110
337 Val Asn Ser Ile Ser Asp Asn Val Trp Glu Val Leu Ile Leu Met Glu
338          115          120          125
339 Tyr Cys Arg Ala Gly Gln Val Val Asn Gln Met Asn Lys Lys Leu Gln
340          130          135          140
341 Thr Gly Phe Thr Glu Ser Glu Val Leu Gln Ile Phe Cys Asp Thr Cys
342 145          150          155          160
343 Glu Ala Val Ala Arg Leu His Gln Cys Lys Thr Pro Ile Ile His Arg
344          165          170          175
345 Asp Leu Lys Val Glu Asn Ile Leu Leu Asn Asp Ala Gly Asn Tyr Val
346          180          185          190
347 Leu Cys Asp Phe Gly Ser Ala Thr Asn Lys Phe Leu Asn Pro Gln Lys
348          195          200          205
349 Asp Gly Val Asn Val Val Glu Glu Glu Ile Lys Lys Tyr Thr Thr Leu
350          210          215          220
351 Ser Tyr Arg Ala Pro Glu Met Ile Asn Leu Tyr Gly Gly Lys Pro Ile
352 225          230          235          240
353 Thr Thr Lys Ala Asp Ile Trp Ala Leu Gly Cys Leu Leu Tyr Lys Leu
354          245          250          255
355 Cys Phe Phe Thr Leu Pro Phe Gly Glu Ser Gln Val Ala Ile Cys Asp
356          260          265          270
357 Gly Ser Phe Thr Ile Pro Asp Asn Ser Arg Tyr Ser His Asn Val His
358          275          280          285
359 Cys Leu Ile Arg Phe Met Leu Glu Pro Asp Pro Glu Cys Arg Pro Asp
360          290          295          300
361 Ile Phe Gln Val Ser Tyr Phe Ala Phe Lys Phe Ala Lys Lys Asp Cys
362 305          310          315          320
363 Pro Val Ser Asn Ile Asn Asn Ser Phe Leu Pro Ser Thr Leu Pro Glu
364          325          330          335
365 Pro Met Thr Ala Thr Glu Ala Ala Ala Arg Lys Ser Gln Met Lys Ala
366          340          345          350
367 Arg Ile Thr Asp Thr Ile Gly Pro Thr Glu Thr Ser Ile Ala Pro Arg
368          355          360          365
369 Gln Arg Pro Lys Ala Asn Ser Thr Ala Ala Thr Ser Ser Val Leu Thr
370          370          375          380
371 Ile Gln Ser Ser Ala Thr Pro Val Lys Val Pro Ala Pro Gly Glu Phe
372 385          390          395          400
373 Ser Asn His Lys Pro Lys Gly Ala Leu Arg Pro Gly Asn Gly Ser Glu
374          405          410          415

```

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```

375 Val Leu Met Val Gln Gly Pro Pro Gln Gln Pro Pro Gln Gln His Arg
376          420          425          430
377 Val Leu Gln Gln Leu Gln Gln Gly Asp Trp Arg Leu Gln Gln Leu His
378          435          440          445
379 Leu His Arg His Pro His His His His Gln Gln Gln Gln Gln Gln Gln
380          450          455          460
381 Gln Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln
382 465          470          475          480
383 Gln Leu Leu Gln Asn Ala Tyr Leu Gln Gln Tyr Gln His Ala Met His
384          485          490          495
385 Gln Gln His Ile Leu Gln Gln Gln Phe Leu Met His Ser Val Tyr Gln
386          500          505          510
387 Pro Gln Pro Pro Ala Ser Gln Tyr Pro Ala Met Met Gln Gln Tyr Gln
388          515          520          525
389 Gln Ala Phe Leu Gln Gln Gln Met Leu Ala Arg His Gln Gln Pro Ala
390          530          535          540
391 Gln Gln Val Ser Pro Glu Tyr Leu Thr Ser Pro Gln Glu Phe Ser Pro
392 545          550          555          560
393 Ala Leu Val Ser Tyr Ala Ser Ser Leu Pro Ala Gln Val Gly Thr Ile
394          565          570          575
395 Val Asp Ser Ser Tyr Gly Ala Asn Arg Ser Val Ala Glu Lys Glu Ala
396          580          585          590
397 Val Ala Asn Phe Thr Asn Gln Lys Thr Ile Ser His Pro Pro Asp Met
398          595          600          605
399 Ser Gly Trp Asn Pro Phe Gly Glu Asp Asn Phe Ser Lys Leu Thr Glu
400          610          615          620
401 Glu Glu Leu Leu Asp Arg Glu Phe Asp Leu Leu Arg Ser Asn Arg Leu
402 625          630          635          640
403 Gly Ala Ser Thr Pro Ser Asp Lys Thr Val Asp Leu Pro Pro Ala Pro
404          645          650          655
405 His Ser Arg Pro Pro Glu Glu Pro Phe Ala Ser Val Pro Phe Ile Ser
406          660          665          670
407 His Ser Gly Ser Pro Glu Lys Lys Thr Thr Glu His Ser Pro Asn Gln
408          675          680          685
409 Lys Ser Ile Thr Ala Asn Leu Thr Lys Asn Gly Gly Ser Ser Pro Leu
410          690          695          700
411 Cys Lys Asp Gln Arg Ala Gly Lys Lys Thr Ser Glu Asn Pro Val Ile
412 705          710          715          720
413 Arg Gly Gln Val Gln Lys Gly His Asp Asp Ser Glu Ser Asp Phe Glu
414          725          730          735
415 Ser Asp Pro Pro Ser Pro Lys Ser Ser Glu Glu Glu Gln Glu Asp Glu
416          740          745          750
417 Asp Ala Gln Gly Glu His Gly Asp Phe Asn Asp Asp Asp Thr Glu Pro
418          755          760          765
419 Glu Asn Leu Gly His Arg Pro Leu Leu Met Asp Ser Glu Asp Glu Glu
420          770          775          780
421 Glu Asp Asp Lys His Ser Ser Asp Ser Glu Cys Glu Gln Ala Lys Thr
422 785          790          795          800
423 Lys Arg Gly Asp Thr Ser Ser Leu Arg Arg Asp Lys Pro Gly Val Ala

```

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```

424          805          810          815
425 Pro Asp Thr Ala Leu Leu Thr Pro Ala Arg Ser Pro Ala Asp Ala Leu
426          820          825          830
427 Thr Pro Ser Gln Glu Phe Asp Val Phe Gly Ala Val Pro Phe Phe Ala
428          835          840          845
429 Ala Pro Ala Pro Gln Ser Leu Gln His Arg Gly Asp Gly Lys Asn Leu
430          850          855          860
431 Ser Gln His Ala Phe Pro Glu Gln Glu Asp Phe Asp Val Phe Thr Lys
432 865          870          875          880
433 Ala Pro Phe Asn Lys Lys Val Ser Val Gln Asp Trp Pro Ala Val Gly
434          885          890          895
435 Pro Asp Ala Arg Pro Leu Pro Ala Arg Pro Arg Ser Val Asp Ile Phe
436          900          905          910
437 Gly Ser Thr Pro Phe Gln Pro Phe Ser Val Ser Ala Ser Lys Ser Glu
438          915          920          925
439 Ser Lys Glu Asp Val Phe Gly Leu Val Pro Phe Glu Glu Ile Thr Gly
440          930          935          940
441 Ser Gln Gln Gln Gln Lys Val Lys Gln Arg Ser Leu Gln Lys Leu Ser
442 945          950          955          960
443 Ser Arg Gln Arg Arg Thr Lys Gln Asp Val Ser Lys Ser Asn Gly Lys
444          965          970          975
445 Arg His His Gly Thr Pro Thr Ser Ala Lys Lys Thr Leu Lys Pro Pro
446          980          985          990
447 Tyr Arg Thr Pro Glu Arg Ala Arg Arg His Lys Lys Val Gly Arg Arg
448          995          1000          1005
449 Asp Ser Gln Ser Ser Asn Glu Phe Leu Thr Ile Ser Asp Ser Lys Glu
450          1010          1015          1020
451 Asn Ile Ser Val Ala Leu Thr Asp Gly Lys Asp Arg Ala Ser Val Leu
452 1025          1030          1035          1040
453 Pro Ser Asp Glu Ser Leu Leu Asp Pro Phe Gly Ala Lys Pro Phe His
454          1045          1050          1055
455 Pro Pro Asp Leu Trp His Gln Pro His Gln Gly Leu Ser Asp Ile Cys
456          1060          1065          1070
457 Val Asp His Thr Thr Ile Leu Pro Gly Arg Pro Arg Gln Asn Ser Val
458          1075          1080          1085
459 His Gly Ser Phe His Ser Ala Glu Thr Leu Arg Met Asp Asp Phe Gly
460          1090          1095          1100
461 Ala Val Pro Phe Thr Glu Leu Val Val Gln Ser Val Thr Pro Gln Gln
462 1105          1110          1115          1120
463 Ser Gln Pro Val Glu Leu Asp Pro Phe Gly Ala Ala Pro Phe Pro Ser
464          1125          1130          1135
465 Lys Gln

```

VERIFICATION SUMMARY

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Input Set : A:\Attorney Docket No. 004974.01054 sequence listing.txt.TXT

Output Set: N:\CRF4\10052004\J509422.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:250 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:4

L:322 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:3